

10/591186

HIRO3010 Sequence Listing
SEQUENCE LISTING

AP18 Rec'd PCT/PTO 30 AUG 2006

<110> Hirasawa, Akira
Tsujimoto, Gozo

<120> Pharmaceutical Composition For Lowering Blood Sugar Level

<130> HIRA3010/REF

<150> JP2004056452

<151> 2004-03-01

<150> JP2004240607

<151> 2004-08-20

<160> 7

<170> PatentIn version 3.1

<210> 1

<211> 377

<212> PRT

<213> Homo sapiens

<400> 1

Met Ser Pro Glu Cys Ala Arg Ala Ala Gly Asp Ala Pro Leu Arg Ser
1 5 10 15

Leu Glu Gln Ala Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys
20 25 30

Gly Asp His Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val
35 40 45

Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
50 55 60

Val Ala Arg Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn
65 70 75 80

Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu
85 90 95

Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His
100 105 110

Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr
115 120 125

Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln
130 135 140

Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala
145 150 155 160

Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe
165 170 175

HIRO3010 Sequence listing

Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser
180 185 190

Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp
195 200 205

Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
210 215 220

Ile Ser Tyr Ser Lys Ile Leu Gln Thr Ser Glu His Leu Leu Asp Ala
225 230 235 240

Arg Ala Val Val Thr His Ser Glu Ile Thr Lys Ala Ser Arg Lys Arg
245 250 255

Leu Thr Val Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
260 265 270

Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
275 280 285

Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
290 295 300

Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
305 310 315 320

Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
325 330 335

Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys
340 345 350

Phe Trp Phe Pro Glu Lys Gly Ala Ile Leu Thr Asp Thr Ser Val Lys
355 360 365

Arg Asn Asp Leu Ser Ile Ile Ser Gly
370 375

<210> 2
<211> 361
<212> PRT
<213> Mus musculus

<400> 2

Met Ser Pro Glu Cys Ala Gln Thr Thr Gly Pro Gly Pro Ser His Thr
1 5 10 15

Leu Asp Gln Val Asn Arg Thr His Phe Pro Phe Phe Ser Asp Val Lys
20 25 30

HIRO3010 Sequence listing

Gly Asp His Arg Leu Val Leu Ser Val Val Glu Thr Thr Val Leu Gly
 35 40 45
 Leu Ile Phe Val Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
 50 55 60
 Val Ala Arg Arg Arg Arg Arg Gly Ala Thr Ala Ser Leu Val Leu Asn
 65 70 75 80
 Leu Phe Cys Ala Asp Leu Leu Phe Thr Ser Ala Ile Pro Leu Val Leu
 85 90 95
 Val Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Val Cys His
 100 105 110
 Leu Leu Phe Tyr Val Met Thr Met Ser Gly Ser Val Thr Ile Leu Thr
 115 120 125
 Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val Arg Leu Arg
 130 135 140
 Arg Gly Leu Ser Gly Pro Gly Arg Arg Thr Gln Ala Ala Leu Leu Ala
 145 150 155 160
 Phe Ile Trp Gly Tyr Ser Ala Leu Ala Ala Leu Pro Leu Cys Ile Leu
 165 170 175
 Phe Arg Val Val Pro Gln Arg Leu Pro Gly Gly Asp Gln Glu Ile Pro
 180 185 190
 Ile Cys Thr Leu Asp Trp Pro Asn Arg Ile Gly Glu Ile Ser Trp Asp
 195 200 205
 Val Phe Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
 210 215 220
 Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
 225 230 235 240
 Leu Thr Leu Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
 245 250 255
 Gln Gln Asp Tyr Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
 260 265 270
 Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
 275 280 285
 Ile Gln Asn Phe Arg Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
 290 295 300

HIRO3010 Sequence listing

Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
305 310 315 320

Tyr Asn Met Ser Leu Phe Arg Asn Glu Trp Arg Lys Ile Phe Cys Cys
325 330 335

Phe Phe Phe Pro Glu Lys Gly Ala Ile Phe Thr Asp Thr Ser Val Arg
340 345 350

Arg Asn Asp Leu Ser Val Ile Ser Ser
355 360

<210> 3
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic DNA

<400> 3
atgtcccctg aatgcgcgcg gg 22

<210> 4
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic DNA

<400> 4
gccagaaata atcgacaagt ca 22

<210> 5
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic DNA

<400> 5
cgcacccgct ttcccttctt ctc 23

<210> 6
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic DNA

<400> 6
agctctttcc ttgatgcctt tgtga 25

<210> 7
<211> 1389
<212> DNA

HIRO3010 Sequence listing

<213> Mus musculus

<400> 7

cagatgagcg ctctctcaga cagcggcggg cggccgggcg cccggcatgt cccctgagtg	60
tgcacagacg acggggccctg gcccctcgca caccctggac caagtcaatc gcacccactt	120
ccctttcttc tcggatgtca agggcgacca ccggttggtg ttgagcgtcg tggagaccac	180
cgttctgggg ctcatctttg tcgtctcact gctgggcaac gtgtgtgctc tagtgctggt	240
ggcgcgccgt cggcgccgtg gggcgacagc cagcctggtg ctcaacctct tctgcgcgga	300
tttgctcttc accagcgcca tccctctagt gctcgtcgtg cgctggactg aggcctggct	360
gttggggccc gtcgtctgcc acctgctctt ctacgtgatg acaatgagcg gcagcgtcac	420
gatactcaca ctggccgcgg tcagcctgga gcgcatggtg tgcacgtgc gcctccggcg	480
cggcttgagc ggcccggggc ggcggactca ggcggcactg ctggctttca tatggggtta	540
ctcggcgctc gccgcgctgc ccctctgcat cttgttccgc gtggtcccgc agcgccttc	600
cggcggggac caggaaattc cgatttgcac attggattgg cccaaccgca taggagaaat	660
ctcatgggat gtgttttttg tgactttgaa cttcctggtg ccgggactgg tcattgtgat	720
cagttactcc aaaattttac agatcacgaa agcatcgcgg aagaggctta cgctgagctt	780
ggcatactct gagagccacc agatccgagt gtcccaacaa gactaccgac tcttccgcac	840
gctcttcctg ctcatggttt ctttcttcat catgtggagt cccatcatca tcaccatcct	900
cctcatcttg atccaaaact tccggcagga cctggtcata tggccatccc ttttcttctg	960
ggtggtggcc ttcacgtttg ccaactctgc cctaaacccc atactgtaca acatgtcgt	1020
gttcaggaac gaatggagga agattttttg ctgcttcttt tttccagaga agggagccat	1080
ttttacagat acgtctgtca ggcgaaatga cttgtctgtt atttccagct aactagcctc	1140
tggtgccagg tgaaccacgg tgtgcatgta aaggaggtta acttcaagga aagcccacca	1200
gtgcgccctg ctttaaaaat acccgacttc caacagcagg catctacgga gccagcaaat	1260
taaggaatga tcgctcagta taaaaatatt tttccttaaa agaactttct atgggttcct	1320
tttgtgaact ttttttagtg tgtttgtaat atgatctagt taataaattt ttatttataa	1380
ctgttccta	1389